REMARKS

A. Background

Claims 1-22 were pending in the application at the time of the Office Action. By this response applicant has amended claims 1, 5, 11, 14, 15, 17, and 18 and cancelled claims 4, 12, and 19-22. As such, claims 1-3, 5-11, and 13-18 are presented to the Examiner for consideration in light of the following remarks.

B. Proposed Claim Amendments

Claims 1, 5, 11, 14, 15, 17, and 18 have been amended herein. Applicant submits that the claim amendments do not introduce new matter and entry thereof is respectfully requested.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached pages are captioned **"Version with Markings to Show Changes Made."**

C. Formal Rejections

Paragraph 2 of the Office Action objected to claims 1, 14, and 17 for failing to include SEQ ID NOS. Applicant has herein amended claims 1, 14,and 17 to include clear reference to the SEQ ID NO in question for each allele. As such, withdrawal of the objections is respectfully requested.

Paragraphs 3 and 4 of the Office Action rejected claims 17 and 19-20 as being non-statutory subject matter. Applicant believes that claim 17 now relates to statutory subject matter in view of its amendment to refer to alleles as being *isolated*, an amendment support by page 15, line 1 below table 1 of the application as filed. Purified alleles are not a product of nature and have no natural occurrence. Such a situation only occurs within a laboratory or the like. Rejected claims 19 and 20

have been cancelled. As such, applicant requests that the rejections under 35 USC §101 be withdrawn.

Paragraphs 5 and 6 of the Office Action rejected claims 1-22 under 35 USC § 112, second paragraph, as being indefinite. In response thereto, claims 1, 14, and 17 have been amended to make clear which of "comprised" or "consists" applies to each of the terms used. Claim 4 has been cancelled. Claim 5 has been amended to clarify that the intention is for seven alleles for each allelic ladder to be present. Claim 11 has been amended to make it clear that the values refer to the allele designation; a concept clearly described in the application and the prior art. Claim 15 has been amended to delete the objected to subject matter. The dependency of claim 18 has been corrected. The examiner was right in his assumption as to the intended dependency. Finally, claims 21 and 22 have been cancelled. In view of the foregoing, applicant respectfully requests that the rejections under 35 USC § 112 be withdrawn.

D. Claim rejections under 35 U.S.C. §102

Paragraphs 7 and 8 of the Office Action rejected Claim 17 under 35 USC 102(a) as being anticipated by Barber. In view of the amendments made herein to claim 17, applicant submits that Barber does not disclose the invention as recited in claim 17. For example, the reference to $(TCTA)_8$ has been deleted. For the other locus, the lowest allele referred to is $(AGAA)_9$ according to Figure 2, not the claimed $(AGAA)_8$.

Paragraph 9 of the Office Action rejected claims 17-18 and 22 under 35 USC 102(a) as being anticipated by Schumm. As previously mentioned, claim 22 has been deleted. With respect to claims 17 and 18, applicant submits that Schumm fails to disclose or suggest the amended alleles recited therein.

In view of the foregoing, applicant respectfully requests that the rejections under 35 USC § 102 be withdrawn.

E. Claim rejections under 35 U.S.C. §103

Paragraphs 10-12 of the Office Action rejected claims 1-8, 10, 14-16, 19-21 under 35 U.S.C. § 103(a) as being unpatentable over Schumm et al. in view of Kimpton et al.

With the amendments made to claims 1 and 14 to specify the sequence the alleles consist of, applicant believes that the claims are now completely free of any suggestion that the claim's definitions include within their scope the alleles referred to in Schumm. As the Examiner acknowledges in the official action, Schumm does not teach the exact alleles recited in claim 1. The concerns that the homology reference lead to a reasonable assertion that Schumm taught allelic ladders as previously defined by claim 1 has been fully addresses. The objected to "ambiguity" in claim 1 has been removed.

Compared with Schumm, for the HUMVWFA31/A locus, the present invention provides 3 alleles not taught by the prior art. Furthermore, there is no suggestion within Schumm that further alleles exist and certainly no suggestion as to their form and sequence. Schumm states that *"Allelic forms of these loci are differentiated by the number of copies of the repeat sequence contained within the amplified region"*, column 1, lines 53-56, and goes on to state, Table 1, column 7, the repeat for this locus is AGAT. It should be noted that the new and inventive alleles for HUMVWFA31/A do not derive their form from this repeat unit. The sequences involved are far more complex. The alleles determined and incorporated into an allelic ladder by the present invention are not implied or pointed towards by the prior art. Instead they represent unpredictable forms.

The alleles and ladders incorporating them are beneficial compared with prior art forms as they allow accurate and rapid characterisation of the size of alleles in unknown samples over a wider range and with more precision within that range.

Compared with Schumm, for the HUMTH01 locus, the present invention provides an allele which is not taught by the prior art. Again the allele is also unexpected when compared with the prior art position, as again it is outside of the range previously suggested and does not arise according to repeats of the AATG repeat referred to in Table 1 of Schumm. Indeed the allele identified in the present invention is not even a 4 base multiple increase on the alleles of Schumm, as the allele is 11 bases larger than the biggest allele in Schumm. This is not a position which could in any way be seen as predictable or pointed towards by Schumm. Again applicant submits that an inventive allele for this locus has been determined and a more useful allelic ladder produced as a result.

Whilst Kimpton et al. does refer to other loci for which STR's can be considered during investigations, it does not provide any details of the alleles at those loci, nor of the use of allelic ladders. As such, Kimpton does not supplement the teaching of Schumm with respect to the HUMVWFA31/A and HUMTH01 loci. Thus, just as Schumm does not teach or suggest the claimed invention with respect to the allelic ladder involving the new and inventive alleles, Kimpton does not change that position. Even if Schumm and Kimpton were combined, the alleles now claimed for the HUMVWFA31/A and HUMTH01 loci would not be taught or suggested by them. Nothing in Kimpton addresses the deficiencies of Schumm, namely that it does not teach or point towards the alleles identities now claimed because it does not suggest those alleles might exist, does not suggest what size those alleles might be and does not suggest the sequence of those alleles. Indeed, as mentioned previously, Schumm's teaching on how alleles vary relative to one another is not the case

with the claimed alleles. In this respect Schumm actually teaches away from the claimed invention. Nothing in Kimpton changes that position.

Given this situation with respect to the HUMVWFA31/A and HUMTH01 loci it cannot reasonably be argued that Schumm and Kimpton in combination teach the allele size and more particularly the allele sequence in respect of the other loci. Kimpton may suggest other loci for use in analysis, but it does not provide any pointers as to the allele sizes which might exist for those loci and more particularly the sequence of those alleles. Schumm itself is also silent on the existence of alleles, size of alleles and sequence of alleles for these loci.

In the circumstances, the applicant respectfully submits that amended claims 1 and 14 are fully novel and inventive over the prior art and are certainly not taught or pointed towards by Schumm and Kimpton.

Claims 19-21 have been cancelled herein and thus the rejection thereto is no longer applicable. The remaining claims 2-8, 10, and 16 depend from claim 1 or 14 and thus incorporate the limitations thereof. As such, applicant submits that claims 2-8, 10, and 16 are distinguished over the cited prior art for at least the same reasons as discussed above with regard to claims 1 and 14.

Furthermore, despite the observations in the Office Action with respect to the dependent claims, applicant believes that the dependent claims also define novel and inventive features over the prior art and particularly the Schumm and Kimpton combination referred to. Given the deficiencies of the prior art against the main allele and allelic ladder claims, even greater gaps exist in the prior art when compared with the more detail and complete allelic ladders in the dependent claims.

Paragraphs 13 and 14 of the Office Action rejected claims 9 and 11 under 35 U.S.C. § 103(a) as being unpatentable over Schumm et al. in view of Kimpton et al. and further in view of Sharma et al. or Barber et al. and Budowle et al. Paragraph 15 of the Office Action stated that

claims 12-13 were objected to as being dependent on a base claim but would be allowable if rewritten to overcome the formal objections and to incorporate the limitations of the base claim.

Claims 9 and 11 depend from claim 1 and thus incorporate the limitations thereof. Applicant submits that claims 9 and 11 are distinguished over the cited prior art for at least the same reasons as discussed above that claim 1 is distinguished over the cited prior art. Furthermore, claim 11 has now been amended to specify a lower and upper weight for each loci. As a consequence, claim 11 now corresponds in subject matter to claim 12 which the Office Action indicated was allowable. Old claim 12 has been deleted. Claim 13 now depends from an allowable claim and as a consequence itself should now be allowable in keeping with paragraph 15 of the Office Action. Claims 11 and 13 thus relate to novel and inventive subject matter.

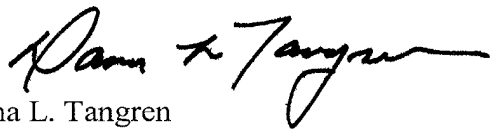
F. Conclusion

In view of the foregoing, applicant respectfully requests the Examiner reconsideration and allowance of claims 1-3, 5-11, and 13-18 as amended and presented herein.

In the event there remains any impediment to allowance of the claims which could be clarified in a telephonic interview, the Examiner is respectfully requested to initiate such an interview with the undersigned.

Dated this 24 day of February 2003.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS

Claims 4, 12, and 19-22 have been cancelled.

Claims 1, 5, 11, 14, 15, 17, and 18 have been amended as set forth below:

1. (Amended) An allelic ladder mixture comprising one or more of the following allelic ladders :-

i) an allelic ladder for locus HUMVWFA31/A comprising one or more [of] alleles [comprising or] consisting of sequences :-

TCTA TCTG TCTA $(TCTG)_4$ $(TCTA)_3$ - SEQ ID NO 1; or

TCTA $(TCTG)_4$ $(TCTA)_7$ - SEQ ID NO 2; or

$(TCTA)_2$ $(TCTG)_4$ $(TCTA)_3$ TCCA $(TCTA)_3$ - SEQ ID NO 3[or at least 75% homologous thereto];

ii) an allelic ladder for locus HUMTHO1 comprising an allele [or] consisting of sequence :-

$(TCAT)_4$ CAT $(TCAT)_7$ TCGT TCAT - SEQ ID NO 4; [or at least 75% homologous thereto;]

iii) an allelic ladder for locus D8S1179 comprising an allele [one or more of alleles] consisting of sequence:-

[$(TCTA)_8$;]

$(TCTA)_2$ TCTG$(TCTA)_{16}$ - SEQ ID NO 6 [or at least 75% homologous thereto];

iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more [of] alleles [comprising or] consisting of [the] sequences :-

$(TTTC)_3$ TTTT TTCT $(CTTT)_5$ T $(CTTT)_3$ CTCC $(TTCC)_2$ - SEQ ID NO 7; or

$(TTTC)_3$ TTTT TTCT $(CTTT)_{13}$ CCTT $(CTTT)_5$ CTCC $(TTCC)_2$ - SEQ ID NO 8; or

$(TTTC)_3$ TTTT TTCT $(CTTT)_{16}$ CCTT $(CTTT)_5$ CTCC $(TTCC)_2$ - SEQ ID NO 9; or

$(TTTC)_4$ TTTT TT $(CTTT)_{15}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 10; or

$(TTTC)_4$ TTTT TT $(CTTT)_{16}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 11; or

$(TTTC)_4$ TTTT TT $(CTTT)_{17}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 12; or

$(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_4$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 13; or

$(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 14; or

$(TTTC)_4$ TTTT TT $(CTTT)_{11}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 15; or

$(TTTC)_4$ TTTT TT $(CTTT)_{10}$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 16; or

$(TTTC)_4$ TTTT TT $(CTTT)_{12}$ $(CTGT)_5$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 17; or

$(TTTC)_4$ TTTT TT $(CTTT)_{14}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 18; [or at least 75% homologous thereto;]

v) an allelic ladder for locus D21S11 comprising one or more [of] alleles [comprising or] consisting of sequences :-

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA$(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_6$ TCGTCT - SEQ ID NO 19; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_9$ TCGTCT - SEQ ID NO 20 or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT - SEQ ID NO 21; or

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_8$ TCGTCT - SEQ ID NO 22; or

$(TCTA)_5$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_9$ TCGTCT - SEQ ID NO 23; or

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT - SEQ ID NO 24; or

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TCGTCT - SEQ ID NO 25; or

$(TCTA)_6$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TCGTCT - SEQ ID NO 26; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 27; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TA TCTA TCGTCT - SEQ ID NO 28; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TA TCTA TCGTCT - SEQ ID NO 29; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{13}$ TA TCTA TCGTCT - SEQ ID NO 30; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{14}$ TATCTA TCGTCT - SEQ ID NO 31; or

$(TCTA)_{10}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 32; or

$(TCTA)_{11}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 33; or

$(TCTA)_{11}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{13}$ TCGTCT - SEQ ID NO 34; or

$(TCTA)_{13}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 35; [or at least 75% homologous thereto;]

vi) an allelic ladder for locus D18S51 comprising an allele [comprising or] consisting of sequence :-

$(AGAA)_8$ - SEQ ID NO 36[; or at least 75% homologous thereto].

2. (Unchanged) An allelic ladder mixture according to claim 1 in which the mixture includes allelic ladders for a plurality of loci selected from HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.

3. (Unchanged) An allelic ladder mixture according to claim 1 the mixture including allelic ladders for at least four loci.

4. (Deleted)

5.(Amended) An allelic ladder mixture according to claim 1 in which the allelic ladders in the mixture <u>each include</u> [includes] at least 7 alleles.

6. (Unchanged) An allelic ladder mixture according to claim 1 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 9 alleles; the HUMTHO1 allelic ladder includes at least 7; the D8S1179 allelic ladder includes at least 9 alleles; the HUMFIBRA/FGA allelic ladder includes at least 18 alleles or is present as HUMFIBRA/FGA/LW and HUMFIBRA/FGA/HW with the HUMFIBRA/FGA/LW ladder including at least 16 alleles, the HUMFIBRA/FGA/HW ladder including at least 6 alleles; the D21S11 allelic ladder includes at least 14 alleles; and the D18S51 ladder includes at least 15 alleles.

7. (Unchanged) An allelic ladder mixture according to claim 1 in which one or more of the allelic ladders in the mixture comprises at least 4 pairs of alleles 4 base pairs from each other.

8. (Unchanged) An allelic ladder mixture according to claim 1 in which the ladders, if present in the mixture, are provided such that: the HUMVWFA31/A allelic ladder includes at least 7 pairs of alleles 4 base pairs from each other; the HUMTHO1 allelic ladder includes at least 5 pairs of alleles 4 base pairs from each other; the D8S1179 allelic ladder includes at least 8 pairs of alleles 4 base pairs from each other; the HUMFIBRA/FGA allelic ladder includes at least 17 pairs of alleles 4 base pairs from each other; the D21S11 allelic ladder includes at least 3 pairs of alleles 4 base pairs from each other; and the D18S51 ladder includes at least 13 pairs of alleles 4 base pairs from each other.

9. (Unchanged) An allelic ladder mixture according to claim 8 in which the D21S11 allelic ladder includes at least 8 pairs of alleles 8 base pairs from each other.

10. (Unchanged) An allelic ladder mixture according to claim 1 in which the ladders, if present, are provided such that the HUMVWFA31/A ladder includes alleles ranging from 130 base pairs upwards and/or from 166 base pairs downwards; the HUMTHO1 ladder includes alleles ranging from 150 base pairs upwards and/or 189 base pairs downwards; the D8S1179 ladder includes alleles ranging from 157 base pairs upwards and/or 201 base pairs downwards; the HUMFIBRA/FGA ladder includes alleles ranging from 173 base pairs upwards and/or 298 base pairs downwards; the D21S11 ladder includes alleles ranging from 203 base pairs upwards and/or 255 base pairs downwards; and the D18S51 ladder includes alleles ranging from 270 base pairs upwards and/or 326 downwards.

11. (Amended) An allelic ladder mixture comprising an allelic ladder for one or more of the following loci, with lowest molecular weight allele and [and/or] uppermost molecular weight allele designation as follows :-

	Locus	Low MW allele Designation	High MW allele Designation
a)	HUMVWFA31/A	10	21
b)	HUMTH01	4	13.3
c)	D8S1179	7	19
d)	HUMFIBRA/FGA	16.1	50.2
e)	D21S11	53	81
f)	D18S51	8	27

12. (Deleted)

13. (Unchanged) An allelic ladder mixture according to claim 11 in which the mixture includes allelic ladders for loci HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 and D18S51.

14. (Amended) A method of analysing one or more samples comprising :-

a) obtaining genomic DNA from the sample;

b) amplifying the DNA;

c) obtaining an indication of one or more of the constituent parts of the sample; and comparing the indications with an allelic ladder mixture comprising one or more of the following allelic ladders :-

i) an allelic ladder for locus HUMVWFA31/A comprising one or more [of] alleles [comprising or] consisting of sequences :-

TCTA TCTG TCTA $(TCTG)_4$ $(TCTA)_3$ - SEQ ID NO 1; or

TCTA $(TCTG)_4$ $(TCTA)_7$ - SEQ ID NO 2; or

$(TCTA)_2$ $(TCTG)_4$ $(TCTA)_3$ TCCA $(TCTA)_3$ - SEQ ID NO 3

ii) an allelic ladder for locus HUMTHO1 comprising an allele [or] consisting of sequence :-

$(TCAT)_4$ CAT $(TCAT)_7$ TCGT TCAT - SEQ ID NO 4;

iii) an allelic ladder for locus D8S1179 comprising an allele [one or more of alleles comprising or] consisting of sequence [sequences]:-

[$(TCTA)_8$; or]

$(TCTA)_2$ TCTG $(TCTA)_{16}$ - SEQ ID NO 6;

iv) an allelic ladder for locus HUMFIBRA/FGA comprising one or more [of] alleles [comprising or] consisting of the sequences :-

$(TTTC)_3$ TTTT TTCT $(CTTT)_5$ T $(CTTT)_3$ CTCC $(TTCC)_2$ - SEQ ID NO 7; or

$(TTTC)_3$ TTTT TTCT $(CTTT)_{13}$ CCTT $(CTTT)_5$ CTCC $(TTCC)_2$ - SEQ ID NO 8; or

$(TTTC)_3$ TTTT TTCT $(CTTT)_{16}$ CCTT $(CTTT)_5$ CTCC $(TTCC)_2$ - SEQ ID NO 9; or

$(TTTC)_4$ TTTT TT $(CTTT)_{15}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 10; or

$(TTTC)_4$ TTTT TT $(CTTT)_{16}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 11; or

$(TTTC)_4$ TTTT TT $(CTTT)_{17}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 12; or

$(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_4$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 13; or

$(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 14; or

$(TTTC)_4$ TTTT TT $(CTTT)_{11}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 15; or

$(TTTC)_4$ TTTT TT $(CTTT)_{10}$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 16; or

$(TTTC)_4$ TTTT TT $(CTTT)_{12}$ $(CTGT)_5$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 17; or

$(TTTC)_4$ TTTT TT $(CTTT)_{14}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 18;

v) an allelic ladder for locus D21S11 comprising one or more [of] alleles [comprising or] consisting of sequences :-

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA$(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_6$ TCGTCT - SEQ ID NO 19; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_9$ TCGTCT - SEQ ID NO 20; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT - SEQ ID NO 21; or

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_8$ TCGTCT - SEQ ID NO 22; or

$(TCTA)_5$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_9$ TCGTCT - SEQ ID NO 23; or

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT - SEQ ID NO 24; or

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TCGTCT - SEQ ID NO 25; or

$(TCTA)_6$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TCGTCT - SEQ ID NO 26; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 27; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TA TCTA TCGTCT - SEQ ID NO 28; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ $_{TA}$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TA TCTA TCGTCT - SEQ ID NO 29; or

$(TCTA)_5$ $(TCTG)_6$ $(_{TCTA})_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{13}$ TA TCTA TCGTCT - SEQ ID NO 30; or

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{14}$ TATCTA TCGTCT - SEQ ID NO 31; or

$(TCTA)_{10}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 32; or

$(TCTA)_{11}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 33; or

$(TCTA)_{11}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{13}$ TCGTCT - SEQ ID NO 34; or

$(TCTA)_{13}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 35;

vi) an allelic ladder for locus D18S51 comprising an allele [comprising or] consisting of sequence :-

$(AGAA)_8$ - SEQ ID NO 36 [;

including allelic ladders or alleles 75% homologous thereto].

15. (Amended) A method according to claim 14 in which the DNA sample is one or more of a sample taken from the scene of a crime, a sample associated with the scene of a crime, a sample obtained from a suspect, a sample obtained from a human under consideration [(for instance for paternity or maternity analysis)] or a reference sample.

16. (Unchanged) A method according to claim 14 in which the sample is amplified using a polymerase chain reaction and primers for one or more of loci HUMVWFA31/A, HUMTHO1, D8S1179, HUMFIBRA/FGA, D21S11 or D18S51 are employed.

17. (Amended) One or more isolated alleles comprising or consisting of sequences

TCTA TCTG TCTA $(TCTG)_4$ $(TCTA)_3$ - SEQ ID NO 1;

TCTA $(TCTG)_4$ $(TCTA)_7$ - SEQ ID NO 2;

$(TCTA)_2$ $(TCTG)_4$ $(TCTA)_3$ TCCA $(TCTA)_3$ - SEQ ID NO 3;

$(TCAT)_4$ CAT $(TCAT)_7$ TCGT TCAT - SEQ ID NO 4;

[$(TCTA)_8$;]

$(TCTA)_2$ TCTG $(TCTA)_{16}$ - SEQ ID NO 6;

$(TTTC)_3$ TTTT TTCT $(CTTT)_5$ T $(CTTT)_3$ CTCC $(TTCC)_2$ - SEQ ID NO 7;

$(TTTC)_3$ TTTT TTCT $(CTTT)_{13}$ CCTT $(CTTT)_5$ CTCC $(TTCC)_2$ - SEQ ID NO 8;

$(TTTC)_3$ TTTT TTCT $(CTTT)_{16}$ CCTT $(CTTT)_5$ CTCC $(TTCC)_2$ - SEQ ID NO 9;

$(TTTC)_4$ TTTT TT $(CTTT)_{15}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 10;

$(TTTC)_4$ TTTT TT $(CTTT)_{16}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 11;

$(TTTC)_4$ TTTT TT $(CTTT)_{17}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 12;

$(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_4$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 13;

$(TTTC)_4$ TTTT TT $(CTTT)_8$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 14;

$(TTTC)_4$ TTTT TT $(CTTT)_{11}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 15;

$(TTTC)_4$ TTTT TT $(CTTT)_{10}$ $(CTGT)_5$ $(CTTT)_{13}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 16;

$(TTTC)_4$ TTTT TT $(CTTT)_{12}$ $(CTGT)_5$ $(CTTT)_{14}$ $(CTTC)_3$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 17;

$(TTTC)_4$ TTTT TT $(CTTT)_{14}$ $(CTGT)_3$ $(CTTT)_{14}$ $(CTTC)_4$ $(CTTT)_3$ CTCC $(TTCC)_4$ - SEQ ID NO 18;

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA$(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_6$ TCGTCT - SEQ ID NO 19;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_9$ TCGTCT - SEQ ID NO 20;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT - SEQ ID NO 21;

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_8$ TCGTCT - SEQ ID NO 22;

$(TCTA)_5$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_9$ TCGTCT - SEQ ID NO 23;

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{10}$ TCGTCT - SEQ ID NO 24;

$(TCTA)_4$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TCGTCT - SEQ ID NO 25;

$(TCTA)_6$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TCGTCT - SEQ ID NO 26;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 27;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{11}$ TA TCTA TCGTCT - SEQ ID NO 28;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TA TCTA TCGTCT - SEQ ID NO 29;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{13}$ TA TCTA TCGTCT - SEQ ID NO 30;

$(TCTA)_5$ $(TCTG)_6$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{14}$ TATCTA TCGTCT - SEQ ID NO 31;

$(TCTA)_{10}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 32;

$(TCTA)_{11}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 33;

$(TCTA)_{11}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{13}$ TCGTCT - SEQ ID NO 34;

$(TCTA)_{13}$ $(TCTG)_5$ $(TCTA)_3$ TA $(TCTA)_3$ TCA $(TCTA)_2$ TCCATA $(TCTA)_{12}$ TCGTCT - SEQ ID NO 35; or

$(AGAA)_8$ - SEQ ID NO 36 [; or at least 75% homologous thereto].

18. (Amended) One or more alleles according to claim 17 [16] in which the alleles are provided purified from alleles other than those of HUMVWFA31/A, HUMTH01, D8S1179, HUMFIBRA/FGA, D21511, D18551 or AMG loci.

19. (Deleted)

20. (Deleted)

21. (Deleted)

22. (Deleted)